<u>IN THE SPECIFICATION</u>:

Please amend the specification to read as follows:

On page 3 replace the paragraph beginning at line 9 which reads "One object..." with the following paragraph:

One object of this invention is to identify and provide a novel and highly conserved protein (referred to hereafter and in the claims as "NGSP") from *Neisseria* spp., preferably *Neisseria gonorrhoeae, Neisseria ovis, Neisseria lacunata, Neisseria osloensis,* and *Neisseria bovis.* The protein of the present invention has a molecular weight of approximately 40-55 kD, and has limited similarity (~36% identity overall) to the DegP (HtrA) protein of *E. coli* [% identity determined using BLASTP Program (Altschul et al., 1990, J. Molec. Biol. 215:403-10; Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402) with data entered using FASTA format; expect 10 filter default; description 100, alignment] and has not been previously identified in any *Neisseria spp.* The protein sequence which is another object of this invention has similarity to several DegP/HtrA-like serine proteases from two other bacteria and these sequence homologies have not been previously reported for any *Neisseria spp.*

On pages 10-11, replace the paragraph starting at page 10, line 15, which reads "The determination of percent identity..." with the following paragraph:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al., 1990, J. Mol.

Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the CGC sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti (1994) Comput. Appl. Biosci., 10:3-5; and FASTA described in Pearson and Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-8. Within FASTA, ktup is a control option that sets the sensitivity and speed of the search. If ktup=2, similar regions in the two sequences being compared are found by looking at pairs of aligned residues; if ktup=1, single aligned amino acids are examined. ktup can be set to 2 or 1 for protein sequences, or from 1 to 6 for DNA sequences. The default if ktup is not specified is 2 for proteins and 6 for DNA.